



RAW SEQUENCE LISTING

DATE: 11/12/2003

PATENT APPLICATION: US/09/581,651B

TIME: 10:27:23

Input Set : A:\35001372.txt

Output Set: N:\CRF4\11122003\I581651B.raw

3 <110> APPLICANT: University of Dundee, University of Dundee
 5 <120> TITLE OF INVENTION: Polypeptides, Polynucleotides and Uses Thereof
 7 <130> FILE REFERENCE: 350013-72
 9 <140> CURRENT APPLICATION NUMBER: 09/581,651B
 10 <141> CURRENT FILING DATE: 2000-10-10
 12 <150> PRIOR APPLICATION NUMBER: PCT/GB98/03766
 13 <151> PRIOR FILING DATE: 1998-12-15
 15 <160> NUMBER OF SEQ ID NOS: 44
 17 <170> SOFTWARE: PatentIn version 3.2
 19 <210> SEQ ID NO: 1
 20 <211> LENGTH: 675
 21 <212> TYPE: PRT
 22 <213> ORGANISM: Homo sapiens
 24 <400> SEQUENCE: 1

ENTERED
P.6

26 Asn Leu Val Ala Thr Cys Leu Pro Val Arg Ala Ser Leu Pro His Arg
 27 1 5 10 15
 30 Leu Asn Met Leu Arg Gly Pro Gly Pro Gly Leu Leu Leu Ala Val
 31 20 25 30
 34 Leu Cys Leu Gly Thr Ala Val Pro Ser Thr Gly Ala Ser Lys Ser Lys
 35 35 40 45
 38 Arg Gln Ala Gln Gln Met Val Gln Pro Gln Ser Pro Val Ala Val Ser
 39 50 55 60
 42 Gln Ser Lys Pro Gly Cys Tyr Asp Asn Gly Lys His Tyr Gln Ile Asn
 43 65 70 75 80
 46 Gln Gln Trp Glu Arg Thr Tyr Leu Gly Asn Val Leu Val Cys Thr Cys
 47 85 90 95
 50 Tyr Gly Gly Ser Arg Gly Phe Asn Cys Glu Ser Lys Pro Glu Ala Glu
 51 100 105 110
 54 Glu Thr Cys Phe Asp Lys Tyr Thr Gly Asn Thr Tyr Arg Val Gly Asp
 55 115 120 125
 58 Thr Tyr Glu Arg Pro Lys Asp Ser Met Ile Trp Asp Cys Thr Cys Ile
 59 130 135 140
 62 Gly Ala Gly Arg Gly Arg Ile Ser Cys Thr Ile Ala Asn Arg Cys His
 63 145 150 155 160
 66 Glu Gly Gly Gln Ser Tyr Lys Ile Gly Asp Thr Trp Arg Arg Pro His
 67 165 170 175
 70 Glu Thr Gly Gly Tyr Met Leu Glu Cys Val Cys Leu Gly Asn Gly Lys
 71 180 185 190
 74 Gly Glu Trp Thr Cys Lys Pro Ile Ala Glu Lys Cys Phe Asp His Ala
 75 195 200 205
 78 Ala Gly Thr Ser Tyr Val Val Gly Glu Thr Trp Glu Lys Pro Tyr Gln
 79 210 215 220
 82 Gly Trp Met Met Val Asp Cys Thr Cys Leu Gly Glu Gly Ser Gly Arg

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83 225                230                235                240
86 Ile Thr Cys Thr Ser Arg Asn Arg Cys Asn Asp Gln Asp Thr Arg Thr
87                245                250                255
90 Ser Tyr Arg Ile Gly Asp Thr Trp Ser Lys Lys Asp Asn Arg Gly Asn
91                260                265                270
94 Leu Leu Gln Cys Ile Cys Thr Gly Asn Gly Arg Gly Glu Trp Lys Cys
95                275                280                285
98 Glu Arg His Thr Ser Val Gln Thr Thr Ser Ser Gly Ser Gly Pro Phe
99    290                295                300
102 Thr Asp Val Arg Ala Ala Val Tyr Gln Pro Gln Pro His Pro Gln Pro
103 305                310                315                320
106 Pro Pro Tyr Gly His Cys Val Thr Asp Ser Gly Val Val Tyr Ser Val
107                325                330                335
110 Gly Met Gln Trp Leu Lys Thr Gln Gly Asn Lys Gln Met Leu Cys Thr
111                340                345                350
114 Cys Leu Gly Asn Gly Val Ser Cys Gln Glu Thr Ala Val Thr Gln Thr
115                355                360                365
118 Tyr Gly Gly Asn Ser Asn Gly Glu Pro Cys Val Leu Pro Phe Thr Tyr
119    370                375                380
122 Asn Gly Arg Thr Phe Tyr Ser Cys Thr Thr Glu Gly Arg Gln Asp Gly
123 385                390                395                400
126 His Leu Trp Cys Ser Thr Thr Ser Asn Tyr Glu Gln Asp Gln Lys Tyr
127                405                410                415
130 Ser Phe Cys Thr Asp His Thr Val Leu Val Gln Thr Gln Gly Gly Asn
131                420                425                430
134 Ser Asn Gly Ala Leu Cys His Phe Pro Phe Leu Tyr Asn Asn His Asn
135                435                440                445
138 Tyr Thr Asp Cys Thr Ser Glu Gly Arg Arg Asp Asn Met Lys Trp Cys
139    450                455                460
142 Gly Thr Thr Gln Asn Tyr Asp Ala Asp Gln Lys Phe Gly Phe Cys Pro
143 465                470                475                480
146 Met Ala Ala His Glu Glu Ile Cys Thr Thr Asn Glu Gly Val Met Tyr
147                485                490                495
150 Arg Ile Gly Asp Gln Trp Asp Lys Gln His Asp Met Gly His Met Met
151    500                505                510
154 Arg Cys Thr Cys Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Tyr Ala
155    515                520                525
158 Tyr Ser Gln Leu Arg Asp Gln Cys Ile Val Asp Asp Ile Thr Tyr Asn
159    530                535                540
162 Val Asn Asp Thr Phe His Lys Arg His Glu Glu Gly His Met Leu Asn
163 545                550                555                560
166 Cys Thr Cys Phe Gly Gln Gly Arg Gly Arg Trp Lys Cys Asp Pro Val
167                565                570                575
170 Asp Gln Cys Gln Asp Ser Glu Thr Gly Thr Phe Tyr Gln Ile Gly Asp
171    580                585                590
174 Ser Trp Glu Lys Tyr Val His Gly Val Arg Tyr Gln Cys Tyr Cys Tyr
175    595                600                605
178 Gly Arg Gly Ile Gly Glu Trp His Cys Gln Pro Leu Gln Thr Tyr Pro
179    610                615                620

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182 Ser Ser Ser Gly Pro Val Glu Val Phe Ile Thr Glu Thr Pro Ser Gln
183 625                      630                      635                      640
186 Pro Asn Ser His Pro Ile Gln Trp Asn Ala Pro Gln Pro Ser His Ile
187                      645                      650                      655
190 Ser Lys Tyr Ile Leu Arg Trp Arg Pro Val Ser Ile Pro Pro Arg Asn
191                      660                      665                      670
194 Leu Gly Tyr
195                      675
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199 <211> LENGTH: 2147
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201 <213> ORGANISM: Homo sapiens
203 <400> SEQUENCE: 2
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206 ttaggggtcc ggggcccggg ctgctgctgc tggcgtcca gtgcctgggg acagcgggtgc      120
208 cctccacggg agcctcgaag agcaagaggc aggcctcagca aatggttcag cccagtcgcc      180
210 cgggtggctgt cagtcaaagc aagcccgggt gttatgacaa tggaaaacac tatcagataa      240
212 atcaacagtg ggagcggacc tacctaggca atgcgttggg ttgtacttgt tatggaggaa      300
214 gccgaggttt taactgcgag agtaaacctg aagctgaaga gacttgcttt gacaagtaca      360
216 ctgggaacac ttaccgagtg ggtgacactt atgagcgtcc taaagactcc atgatctggg      420
218 actgtacctg catcggggct gggcgaggga gaataagctg taccatcgca aaccgctgcc      480
220 atgaaggggg tcagtcctac aagattgggt acacctggag gagaccacat gagactggtg      540
222 gttacatggt agagtgtgtg tgtcttggtg atggaaaagg agaatggacc tgcaagccca      600
224 tagctgagaa gtgttttgat catgctgctg ggacttccta tgtggtcgga gaaacgtggg      660
226 agaagcccta ccaaggctgg atgatggtag attgtacttg cctgggagaa ggcagcggac      720
228 gcatcacttg cacttctaga aatagatgca acgatcagga cacaaggaca tcctatagaa      780
230 ttggagacac ctggagcaag aaggataatc gaggaaacct gctccagtgc atctgcacag      840
232 gcaacggccg aggagagtgg aagtgtgaga ggcacacctc tgtgcagacc acatcgagcg      900
234 gatctggccc cttcaccgat gttcgtgcag ctgtttacca accgcagcct cccccccagc      960
236 ctctcccta tggccactgt gtcacagaca gtggtgtggt ctactctgtg gggatgcagt      1020
238 ggctgaagac acaaggaaat aagcaaatgc tttgcacgtg cctgggcaac ggagtcagct      1080
240 gccaaagac agctgtaacc cagacttacg gtggcaactc aaatggagag ccatgtgtct      1140
242 taccattcac ctacaacgac aggacggaca gcacaacttc gaattatgag caggaccaga      1200
244 aatactcttt ctgcacagac cacactgttt tgggttcagac tcgaggagga aattccaatg      1260
246 gtgccttggt ccacttcccc ttctataca acaaccacaa ttactatgat tgcacttctg      1320
248 agggcagaag agacaacatg aagtgggtgt ggaccacaca gaactatgat gccgaccaga      1380
250 agtttggttt ctgccccatg gctgcccacg aggaaatctg cacaaccaat gaaggggtca      1440
252 tgtaccgcat tggagatcag tgggataagc agcatgacat gggtcacatg atgaggtgca      1500
254 cgtgtgttgg gaatggtcgt ggggaatgga catgcattgc ctactcgag cttcgagatc      1560
256 agtgcattgt tgatgacatc acttacaatg tgaacgacac attccacaag cgtcatgaag      1620
258 aggggcacat gctgaactgt acatgcttcg gtcagggctg gggcaggtgg aagtgtgatc      1680
260 ccgtcgacca atgccaggat tcagagactg ggacgtttta tcaaattgga gattcatggg      1740
262 agaagtatgt gcatggtgtc agataccagt gctactgcta tggcgtggc attggggagt      1800
264 ggcattgcca acctttacag acctatcaa gctcaagtgg tcctgtcgaa gtatttatca      1860
266 ctgagactcc gagtcagccc aactcccacc ccctccagtg gaatgcacca cagccatctc      1920
268 acatttccaa gtacattctc aggtggagac ctgtgagtat cccaccaga aaccttggat      1980
270 actgagtctc ctaatcttat caattctgat ggtttctttt tttcccagct tttgagccaa      2040
272 caactctgat taactattcc tatagcattt actatatttg tttagtgaac aaacaatatg      2100
274 tggtaatta aattgacttg tagactgaaa aaaaaaaaaa aaaaaaa      2147

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277 <210> SEQ ID NO: 3
278 <211> LENGTH: 20
279 <212> TYPE: PRT
280 <213> ORGANISM: Homo sapiens
282 <400> SEQUENCE: 3
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288 Asn Leu Gly Tyr
289 20
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293 <211> LENGTH: 21
294 <212> TYPE: PRT
295 <213> ORGANISM: Homo sapiens
297 <400> SEQUENCE: 4
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303 Tyr Gly Gly Ser Arg
304 20
307 <210> SEQ ID NO: 5
308 <211> LENGTH: 23
309 <212> TYPE: PRT
310 <213> ORGANISM: Homo sapiens
312 <400> SEQUENCE: 5
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315 1 5 10 15
318 Ser Asn Tyr Glu Gln Asp Gln
319 20
322 <210> SEQ ID NO: 6
323 <211> LENGTH: 20
324 <212> TYPE: PRT
325 <213> ORGANISM: Homo sapiens
327 <400> SEQUENCE: 6
329 Thr Asp His Thr Val Leu Val Gln Thr Arg Gly Gly Asn Ser Asn Gly
330 1 5 10 15
333 Ala Leu Cys His
334 20
337 <210> SEQ ID NO: 7
338 <211> LENGTH: 21
339 <212> TYPE: PRT
340 <213> ORGANISM: Homo sapiens
342 <400> SEQUENCE: 7
344 Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Ile Ala Tyr Ser Gln Leu
345 1 5 10 15
348 Arg Asp Gln Cys Ile
349 20
352 <210> SEQ ID NO: 8
353 <211> LENGTH: 21
354 <212> TYPE: PRT
355 <213> ORGANISM: Homo sapiens

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TIME: 10:27:23

Input Set : A:\35001372.txt

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357 <400> SEQUENCE: 8
359 Gln Gln Trp Glu Arg Thr Tyr Leu Gly Asn Val Leu Val Cys Thr Cys
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363 Tyr Gly Gly Ser Arg
364 20
367 <210> SEQ ID NO: 9
368 <211> LENGTH: 39
369 <212> TYPE: PRT
370 <213> ORGANISM: Homo sapiens
372 <400> SEQUENCE: 9
374 Glu Pro Cys Val Leu Pro Phe Thr Tyr Asn Gly Arg Thr Phe Tyr Ser
375 1 5 10 15
378 Cys Thr Thr Glu Gly Arg Gln Asp Gly His Leu Trp Cys Ser Thr Thr
379 20 25 30
382 Ser Asn Tyr Glu Gln Asp Gln
383 35
386 <210> SEQ ID NO: 10
387 <211> LENGTH: 21
388 <212> TYPE: PRT
389 <213> ORGANISM: Homo sapiens
391 <400> SEQUENCE: 10
393 Cys Thr Asp His Thr Val Leu Val Gln Thr Gln Gly Gly Asn Ser Asn
394 1 5 10 15
397 Gly Ala Leu Cys His
398 20
401 <210> SEQ ID NO: 11
402 <211> LENGTH: 21
403 <212> TYPE: PRT
404 <213> ORGANISM: Homo sapiens
406 <400> SEQUENCE: 11
408 Val Gly Asn Gly Arg Gly Glu Trp Thr Cys Thr Ala Tyr Ser Gln Leu
409 1 5 10 15
412 Arg Asp Gln Cys Ile
413 20
416 <210> SEQ ID NO: 12
417 <211> LENGTH: 20
418 <212> TYPE: PRT
419 <213> ORGANISM: Homo sapiens
421 <400> SEQUENCE: 12
423 Ile Ser Lys Thr Ile Leu Arg Trp Arg Pro Lys Asn Ser Val Gly Arg
424 1 5 10 15
427 Trp Lys Glu Ala
428 20
431 <210> SEQ ID NO: 13
432 <211> LENGTH: 18
433 <212> TYPE: PRT
434 <213> ORGANISM: Homo sapiens
436 <400> SEQUENCE: 13
438 Asn Leu Val Ala Thr Cys Leu Pro Val Arg Ala Ser Leu Pro His Arg

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RAW SEQUENCE LISTING ERROR SUMMARY
PATENT APPLICATION: US/09/581,651B

DATE: 11/12/2003
TIME: 10:27:24

Input Set : A:\35001372.txt
Output Set: N:\CRF4\11122003\I581651B.raw

ase Note:

of n and/or Xaa have been detected in the Sequence Listing. Please review the
uence Listing to ensure that a corresponding explanation is presented in the <220>
<223> fields of each sequence which presents at least one n or Xaa.

#:37; Xaa Pos. 676,679,683,717